

The Material of Heredity

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Nucleic Acids

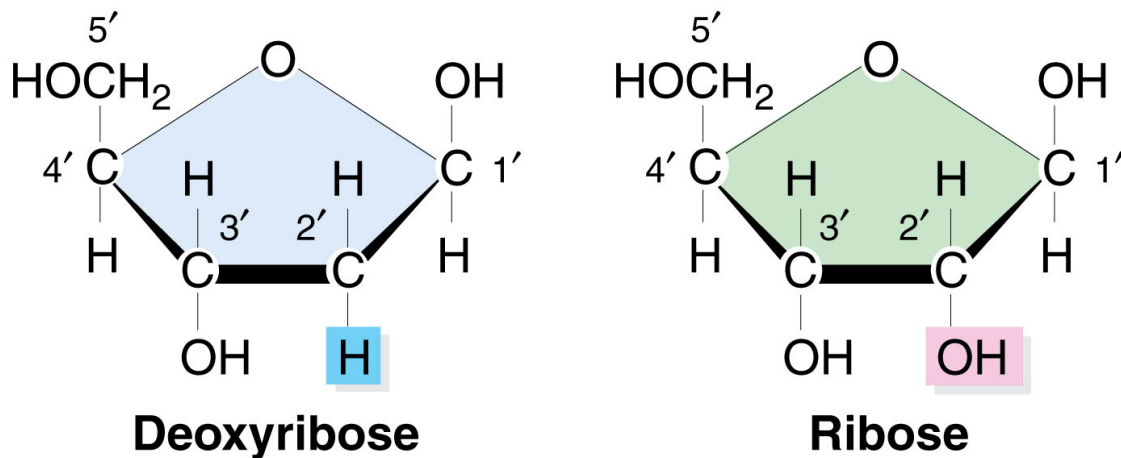
In the early 1900's it was discovered that nucleic acids were an important component of chromosomes

Levene isolated two types of nucleic acids (based on their sugar composition)

- one contained the five carbon sugar ribose (ribose nucleic acid = ribonucleic acid or RNA)

- the other contained a ribose sugar that was missing one oxygen (deoxyribose = deoxyribonucleic acid or DNA)

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Nucleic acids are made up of long chains of individual units called nucleotides.

Both DNA and RNA are made up of four different nucleotides.

Each nucleotide is composed of a five-carbon sugar, a phosphate group and one of four nitrogen bases.

Nitrogen Bases Of DNA:

Adenine (A)

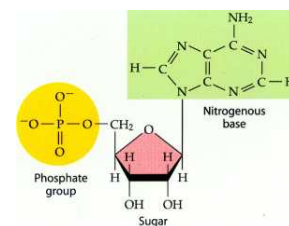
Thymine (T)

Guanine (G)

Cytosine (C)

(purines)

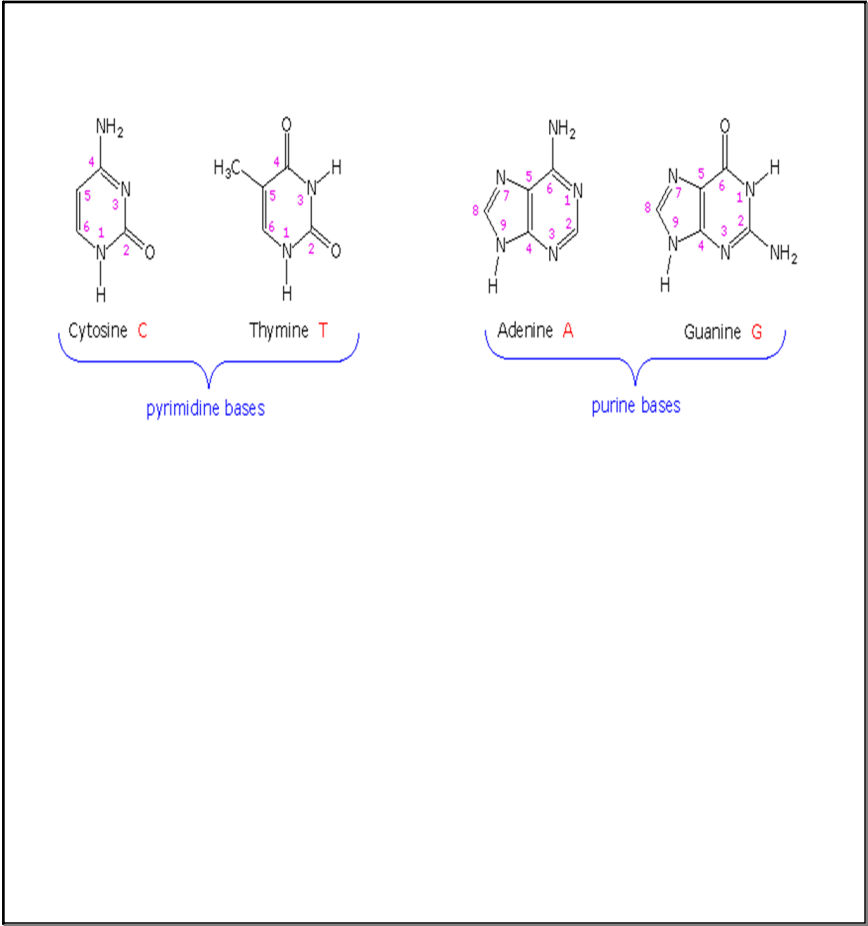
(pyrimidines)



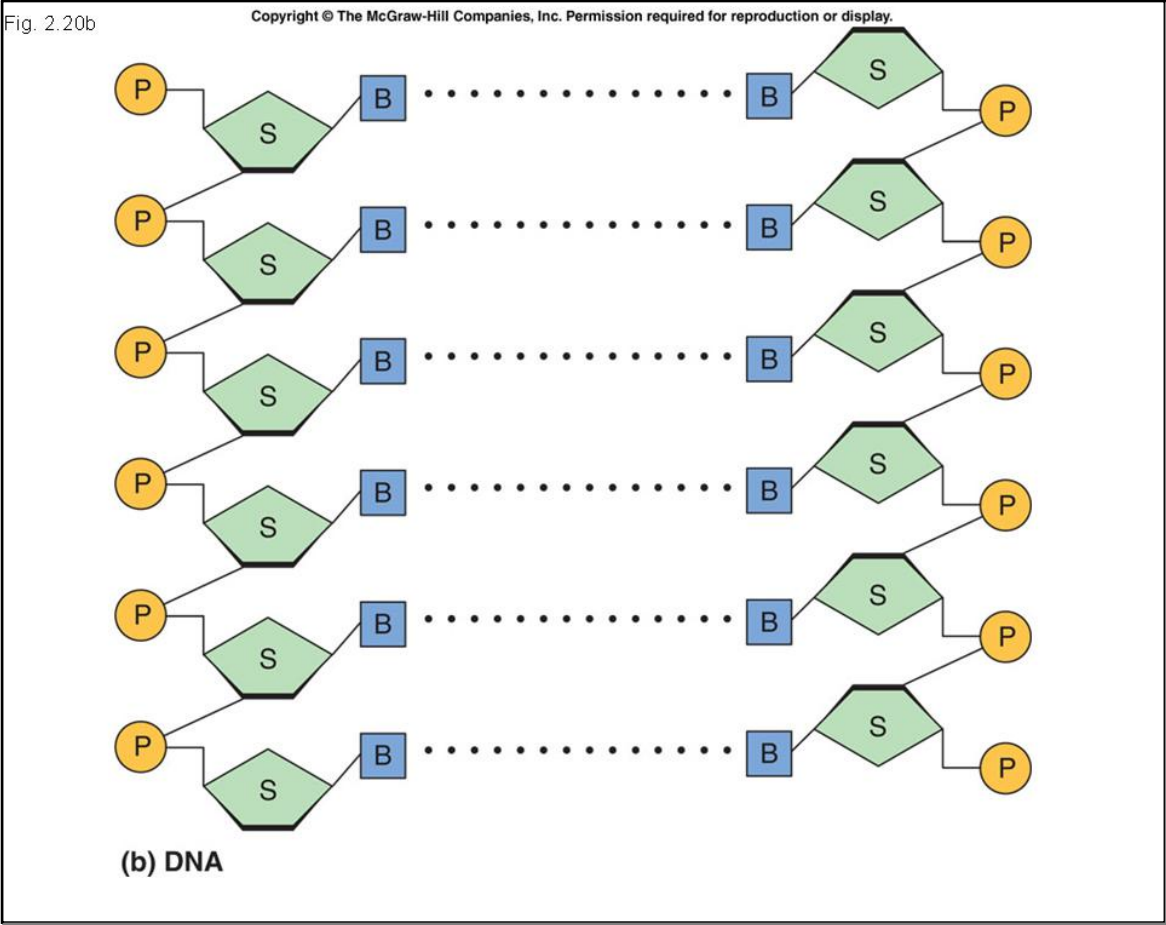
In RNA Uracil (U) replaces Thymine

Note each DNA triplet codes for one amino acid.

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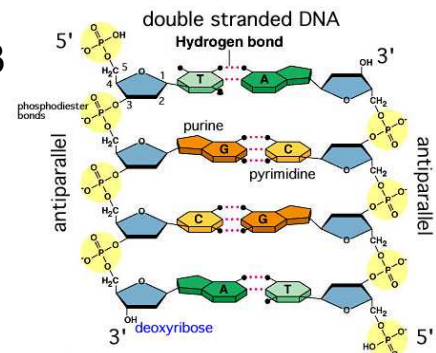
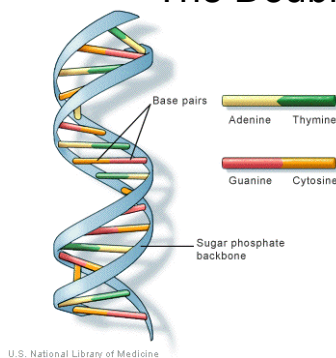
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The Structure of DNA

Rosalind Franklin was able to identify the helical structure of DNA in the 1950's, using x ray technology. However because of the prevailing attitudes toward women in science her work was not widely recognized

James Watson and Francis Crick were the first to produce a structural model of DNA that was accepted by the science community.

- The Double Helix Model ~ 1953



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DNA and RNA

- Are both found in most bacteria as well as eukaryotic cell nuclei.
- Have similar structures with the exception that RNA has
 - ribose instead of a deoxyribose sugar
 - Uracil replaces Thymine
 - RNA is single stranded that can fold back on itself to produce regions of complementary base pairs.

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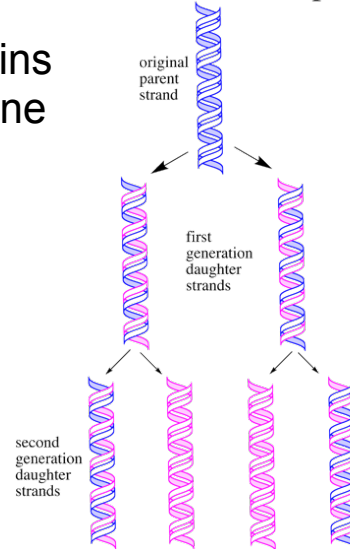
DNA Replication

During DNA replication two molecules of DNA are made from one.

Uses a semi-conservative model

- each new molecule of DNA contains one strand of parental DNA and one strand of new DNA

Semiconservative Replication



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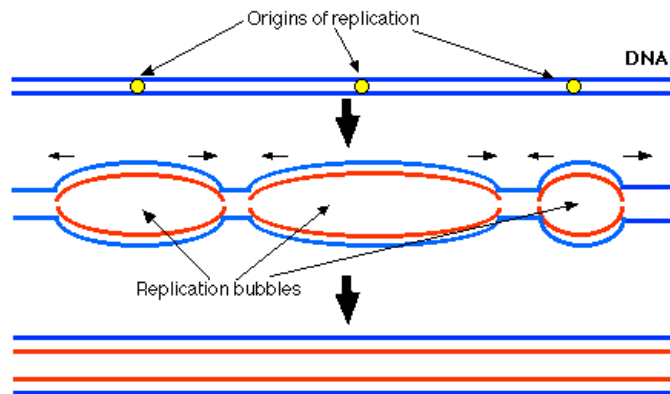
3 Main Stages of Replication

1. Initiation
2. Elongation
3. Termination

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Initiation

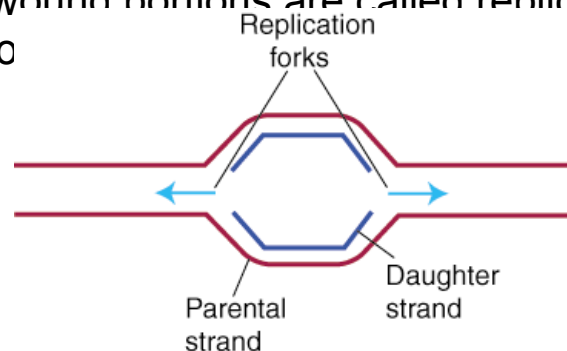
- On a single strand replication can be initiated at hundreds of replication origins.
- **Replication origin** - nucleotide sequence of 100- 200 base pairs that is recognized by an enzyme that forces the DNA to separate and create a replication bubble.



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Unwinding the Helix

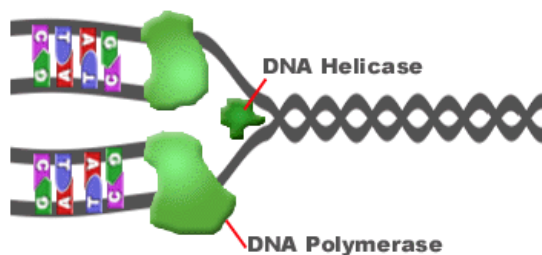
- the helix must be unwound in order for the individual chains of nucleotides to serve as templates for the formation of new strands
- Helicase is the enzyme responsible for unraveling the DNA
- These unwound portions are called replication forks (one at each end of the bubble)



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DNA Polymerase

- inserts itself into the replication bubble
- uses the parent strand as a template to add nucleotides one at a time
- creates a complementary new strand

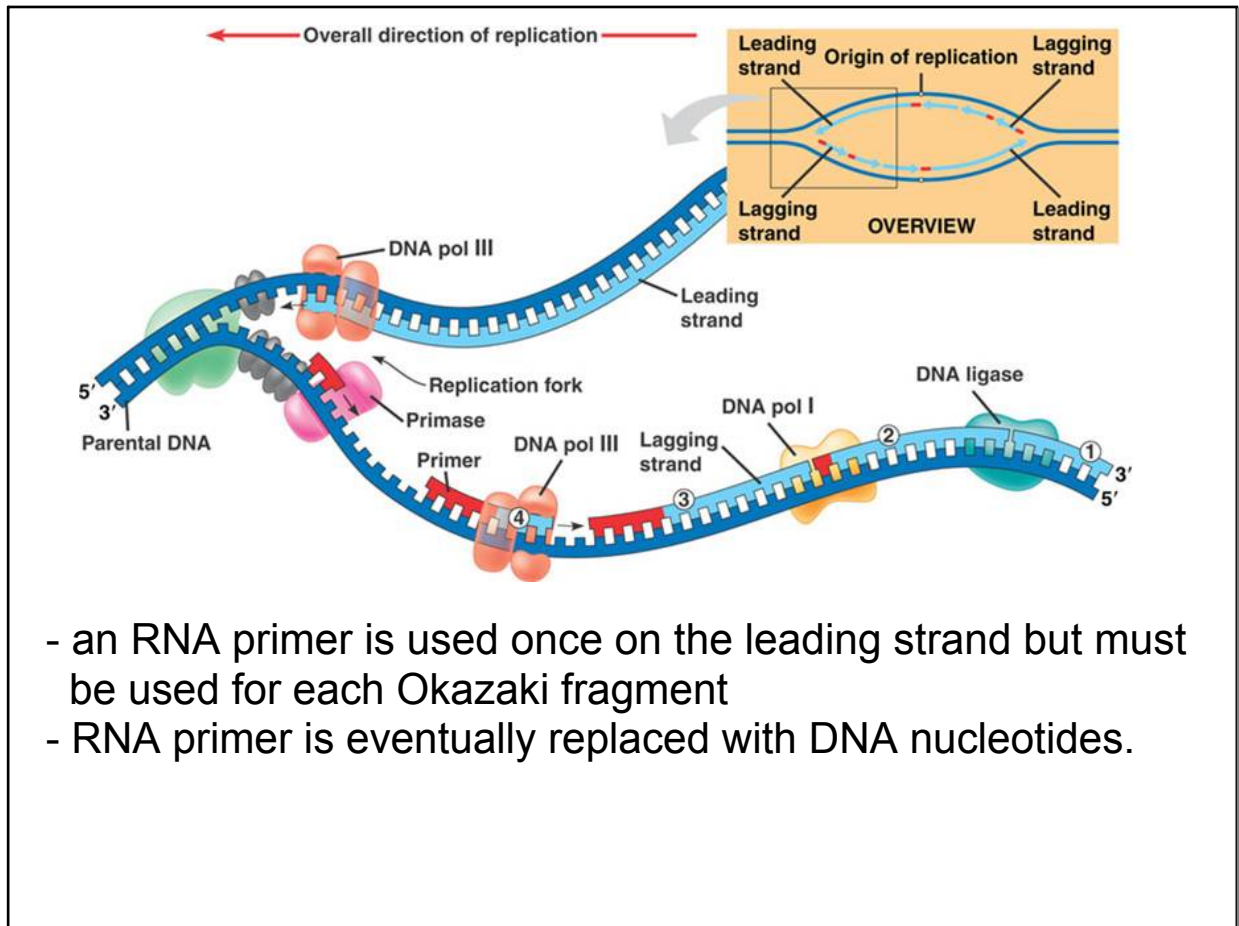


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ELONGATION

- polymerase will only allow replication to take place in the 5' to 3' direction
 - creates a leading and a lagging strand of DNA
 - leading strand is replicated continuously following the replication fork
 - lagging strand is made in short pieces moving away from the replication fork
- **Okazaki fragments** are created on the lagging strand (daughter strand that must be built in the 3' to 5' direction). The fragments are spliced together using an enzyme called **DNA ligase**

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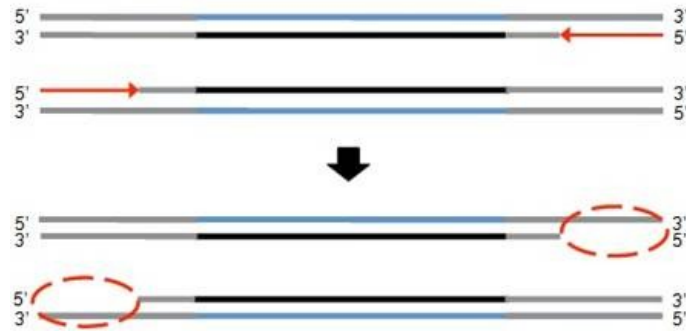
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- Replication continues until all the replication bubbles have met and the two new DNA molecules separate from each other.

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TERMINATION

- with each replication more DNA is lost due to the removal of the RNA primer from the 5' end of each daughter strand
- about 100 base pairs from the ends of each chromosome with each replication



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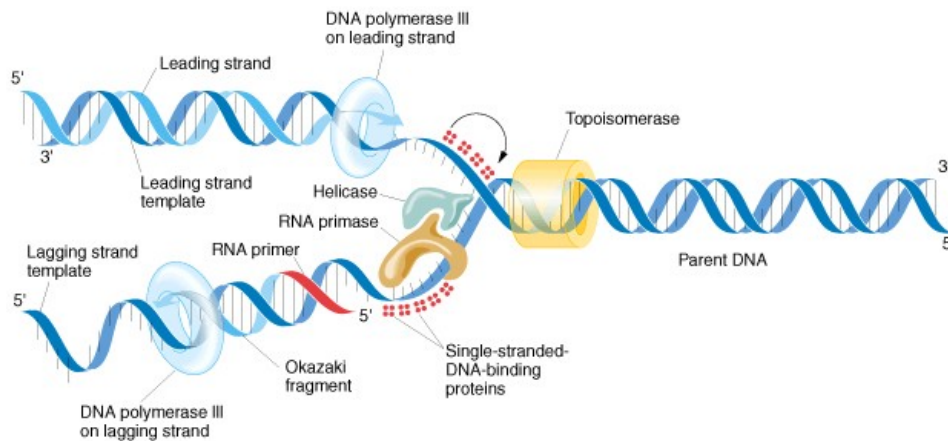
Telomeres

- stretches of highly repetitive nucleotide sequences that guard against the loss of vital genetic information during the replication process
- human typical nucleotide sequence is TTAGGG (repeated several thousand times)
- erosion of the telomeres = cell death
 - **telomerase** - enzyme that extends telomeres (seen in cancer cells)

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Proofreading and Correction

- sometimes during the replication process the wrong base can be inserted. (1 error in every 10 000-100 000 bases)
- a mismatch is recognized when hydrogen bonding between bases does not occur and polymerase excises the incorrect base and inserts the proper base.



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